



Bayer Aktiengesellschaft

<120> Nucleic Acids which encode
insect acetylcholine receptor subunits

<130> Le A 33 020-Foreign Countries

<140> US/09/303,232

<141> 1999-04-30

<150> DE 198 19 829.9

<151> 1998-05-04

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<170> PatentIn Ver. 2.1

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Asp Glu Leu Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe
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Ser Ser Ser Ser Ser Thr Arg Thr Thr Ser Ser Asn Gln Arg His Asn
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Gln Gln Leu Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His
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Thr His Leu Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr
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gcc gca gca gca act gct gcc ggc gat gaa gca aca acc caa caa cca 746
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His Ile Ile Val Ser
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Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser Ser Ser Ser
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Trp Pro Arg Gly Ala Arg Cys Gly Tyr His Glu Lys Arg Leu Leu His
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<213> *Heliothis virescens*

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His Glu Lys Arg Leu Leu His His Leu Leu Asp His Tyr Asn Val Leu
35 40 45

Glu Arg Pro Val Val Asn Glu Ser Asp Pro Leu Gln Leu Ser Phe Gly
50 55 60

Leu Thr Leu Met Gln Ile Ile Asp Val Asp Glu Lys Asn Gln Leu Leu
65 70 75 80

Ile Thr Asn Ile Trp Leu Lys Leu Glu Trp Asn Asp Met Asn Leu Arg
85 90 95

Trp Asn Thr Ser Asp Phe Gly Gly Val Lys Asp Leu Arg Val Pro Pro
100 105 110

His Arg Leu Trp Lys Pro Asp Val Leu Met Tyr Asn Ser Ala Asp Glu
115 120 125

Gly Phe Asp Ser Thr Tyr Pro Thr Asn Val Val Val Arg Asn Asn Gly
130 135 140

Ser Cys Leu Tyr Val Pro Pro Gly Ile Phe Lys Ser Thr Cys Lys Ile
145 150 155 160

Asp Ile Thr Trp Phe Pro Phe Asp Asp Gln Arg Cys Glu Met Lys Phe
165 170 175

Gly Ser Trp Thr Tyr Asp Gly Tyr Gln Leu Asp Leu Gln Leu Gln Asp
180 185 190

Glu Gly Gly Gly Asp Ile Ser Ser Phe Val Thr Asn Gly Glu Trp Glu
195 200 205

Leu Ile Gly Val Pro Gly Lys Arg Asn Glu Ile Tyr Tyr Asn Cys Cys
210 215 220

Pro Glu Pro Tyr Ile Asp Ile Thr Phe Ala Val Val Ile Arg Arg Lys
225 230 235 240

Thr Leu Tyr Tyr Phe Phe Asn Leu Ile Val Pro Cys Val Leu Ile Ala
245 250 255

Ser Met Ala Leu Leu Gly Phe Thr Leu Pro Pro Asp Ser Gly Glu Lys
260 265 270

Leu Ser Leu Gly Val Thr Ile Leu Leu Ser Leu Thr Val Phe Leu Asn
275 280 285

Met Val Ala Glu Thr Met Pro Ala Thr Ser Asp Ala Val Pro Leu Leu
290 295 300

Gly Thr Tyr Phe Asn Cys Ile Met Phe Met Val Ala Ser Ser Val Val
305 310 315 320

Ser Thr Ile Leu Ile Leu Asn Tyr His His Arg His Ala Asp Thr His
325 330 335

Glu Met Ser Asp Trp Ile Arg Cys Val Phe Leu Tyr Trp Leu Pro Trp
340 345 350

Val Leu Arg Met Ser Arg Pro Gly Ser Ala Thr Thr Pro Pro Pro Ala
355 360 365

Arg Val Pro Pro Pro Pro Asp Leu Glu Leu Arg Glu Arg Ser Ser Lys
370 375 380

Ser Leu Leu Ala Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Pro
385 390 395 400

Gln Ala Gln Gln Pro Gln Cys Cys Arg Tyr Tyr Arg Gly Gly Glu Glu
405 410 415

Asn Gly Ala Gly Leu Ala Ala His Ser Cys Phe Gly Val Asp Tyr Glu
420 425 430

Leu Ser Leu Ile Leu Lys Glu Ile Arg Val Ile Thr Asp Gln Met Arg
435 440 445

Lys Asp Asp Glu Asp Ala Asp Ile Ser Arg Asp Trp Lys Phe Ala Ala
450 455 460

Met Val Val Asp Arg Leu Cys Leu Ile Ile Phe Thr Leu Phe Thr Ile
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Ile Ala Thr Leu Ala Val Leu Leu Ser Ala Pro His Ile Met Val Ser
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Met Ala Pro Met Leu Ala Ala
1 5

ttg gcg ctg ctg gct ttg ctg ccc gta tcg gag caa ggt cct cac gag 163
Leu Ala Leu Leu Ala Leu Leu Pro Val Ser Glu Gln Gly Pro His Glu
10 15 20

aag aga ctc ctg aac gcg ttg ctg gcg aac tac aac acc ctg gag cga 211
Lys Arg Leu Leu Asn Ala Leu Leu Ala Asn Tyr Asn Thr Leu Glu Arg
25 30 35

ccg gtg gcc aac gag agc gaa ccg cta gag gtc agg ttc ggc ttg acc 259
Pro Val Ala Asn Glu Ser Glu Pro Leu Glu Val Arg Phe Gly Leu Thr
40 45 50 55

ttg cag caa atc att gac gtg gac gag aag aat caa cta ctt ata acc 307
Leu Gln Gln Ile Ile Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr
60 65 70

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aat ata tgg ctg tcg ttg gag tgg aat gac tac aac ctg agg tgg aac 355
Asn Ile Trp Leu Ser Leu Glu Trp Asn Asp Tyr Asn Leu Arg Trp Asn
75 80 85

gac agc gag tat ggc ggg gtc aag gac ctc agg atc acg ccc aac aag 403
Asp Ser Glu Tyr Gly Gly Val Lys Asp Leu Arg Ile Thr Pro Asn Lys
90 95 100

ttg tgg aag ccg gac gtc ctt atg tat aat agt gct gac gag ggt ttt 451
Leu Trp Lys Pro Asp Val Leu Met Tyr Asn Ser Ala Asp Glu Gly Phe
105 110 115

gac ggg acc tac cag acc aac gtg gtg gtc aga agc ggc ggc agt tgc 499
Asp Gly Thr Tyr Gln Thr Asn Val Val Val Arg Ser Gly Gly Ser Cys
120 125 130 135

ctg tac gtg cca cct ggc ata ttc aag agc aca tgc aag atg gac atc 547
Leu Tyr Val Pro Pro Gly Ile Phe Lys Ser Thr Cys Lys Met Asp Ile
140 145 150

gcg tgg ttt ccc ttc gac gac caa cac tgt gat atg aag ttc ggt agc 595
Ala Trp Phe Pro Phe Asp Asp Gln His Cys Asp Met Lys Phe Gly Ser
155 160 165

tgg aca tat gac ggc aat cag ttg gat ctg gtg cta aaa gat gag gca 643
Trp Thr Tyr Asp Gly Asn Gln Leu Asp Leu Val Leu Lys Asp Glu Ala
170 175 180

ggc ggc gat cta tcg gac ttc ata aca aat ggg gag tgg tat cta ata 691
Gly Gly Asp Leu Ser Asp Phe Ile Thr Asn Gly Glu Trp Tyr Leu Ile
185 190 195

gga atg cca ggc aaa aag aac aca ata aca tac gcg tgc tgc ccc gag 739
Gly Met Pro Gly Lys Lys Asn Thr Ile Thr Tyr Ala Cys Cys Pro Glu
200 205 210 215

ccc tac gtg gac gtc acc ttc acc atc atg ata aga aga cga acc ttg 787
Pro Tyr Val Asp Val Thr Phe Thr Ile Met Ile Arg Arg Arg Thr Leu
220 225 230

tac tac ttc ttc aac ctg atc gtc ccg tgc gtg ctg atc tca tcg atg 835
Tyr Tyr Phe Phe Asn Leu Ile Val Pro Cys Val Leu Ile Ser Ser Met
235 240 245

gca ctc ctc ggc ttc aca ctg cca cca gac tcc gga gag aaa ctc aca 883
Ala Leu Leu Gly Phe Thr Leu Pro Pro Asp Ser Gly Glu Lys Leu Thr
250 255 260

ctt gga gtc act att ctt cta tcg ctg acg gtg ttc ctc aac ctg gta 931
Leu Gly Val Thr Ile Leu Leu Ser Leu Thr Val Phe Leu Asn Leu Val
265 270 275

gcc gag acc ctg cca cag gtc tcc gac gct atc ccc ctg tta ggg acg 979
Ala Glu Thr Leu Pro Gln Val Ser Asp Ala Ile Pro Leu Leu Gly Thr
280 285 290 295

tac ttc aat tgc atc atg ttc atg gta gcg tcg tct gtg gta ctg act 1027
 Tyr Phe Asn Cys Ile Met Phe Met Val Ala Ser Ser Val Val Leu Thr
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gtg gtg gta ctc aat tac cac cat cga aca gct gat ata cat gaa atg 1075
 Val Val Val Leu Asn Tyr His His Arg Thr Ala Asp Ile His Glu Met
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cca cag tgg ata aaa tca gta ttc cta caa tgg ttg cca tgg ata ctg 1123
 Pro Gln Trp Ile Lys Ser Val Phe Leu Gln Trp Leu Pro Trp Ile Leu
 330 335 340

cga atg tcg agg cca ggg aag aag atc acc agg aag act ata atg atg 1171
 Arg Met Ser Arg Pro Gly Lys Lys Ile Thr Arg Lys Thr Ile Met Met
 345 350 355

aac acg agg atg agg gag ctg gaa ctg aag gag agg tcg tcg aag tcc 1219
 Asn Thr Arg Met Arg Glu Leu Glu Leu Lys Glu Arg Ser Ser Lys Ser
 360 365 370 375

B1
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 380 385 390

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 Pro Pro Pro Asn Ser Thr Ala Ser Thr Gly Asn Leu Gly Pro Gly Cys
 395 400 405

tca ata ttc cgc acg gat ttc cgt cgg tcg ttc gtc cgt ccg tcc acg 1363
 Ser Ile Phe Arg Thr Asp Phe Arg Arg Ser Phe Val Arg Pro Ser Thr
 410 415 420

atg gaa gac gtg ggc ggc ggg ctg ggt agc cac cat cgc gag ctg cac 1411
 Met Glu Asp Val Gly Gly Gly Leu Gly Ser His His Arg Glu Leu His
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ctc ata ctg aga gag ctg cag ttc atc acg gcc agg atg aag aag gct 1459
 Leu Ile Leu Arg Glu Leu Gln Phe Ile Thr Ala Arg Met Lys Lys Ala
 440 445 450 455

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 Asp Glu Glu Ala Glu Leu Ile Ser Asp Trp Lys Phe Ala Ala Met Val
 460 465 470

gtt gat agg ttt tgc ctg ttc gtg ttc aca ctt ttc aca atc atc gcg 1555
 Val Asp Arg Phe Cys Leu Phe Val Phe Thr Leu Phe Thr Ile Ile Ala
 475 480 485

aca gta gct gtc ctg tta tcg gca ccg cat atc atc gtg caa 1597
 Thr Val Ala Val Leu Leu Ser Ala Pro His Ile Ile Val Gln
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tgaaccaacc actgagccgg caactccggc gcatgaatga gagaaataat tattagatcg 1657

ccgatttgta attataattg ataatgtaat taaattaaat acgtggttga aacgcacacg 1717

tctccataac aaagtcttaa gacattaaat tatgataaat ttacatattg tagttaagtc 1777

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35 40 45

Glu Val Arg Phe Gly Leu Thr Leu Gln Gln Ile Ile Asp Val Asp Glu
50 55 60

Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Ser Leu Glu Trp Asn
65 70 75 80

Asp Tyr Asn Leu Arg Trp Asn Asp Ser Glu Tyr Gly Gly Val Lys Asp
85 90 95

Leu Arg Ile Thr Pro Asn Lys Leu Trp Lys Pro Asp Val Leu Met Tyr
100 105 110

Asn Ser Ala Asp Glu Gly Phe Asp Gly Thr Tyr Gln Thr Asn Val Val
115 120 125

Val Arg Ser Gly Gly Ser Cys Leu Tyr Val Pro Pro Gly Ile Phe Lys
130 135 140

Ser Thr Cys Lys Met Asp Ile Ala Trp Phe Pro Phe Asp Asp Gln His
145 150 155 160

Cys Asp Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Asn Gln Leu Asp
165 170 175

Leu Val Leu Lys Asp Glu Ala Gly Gly Asp Leu Ser Asp Phe Ile Thr
180 185 190

Asn Gly Glu Trp Tyr Leu Ile Gly Met Pro Gly Lys Lys Asn Thr Ile
195 200 205

Thr Tyr Ala Cys Cys Pro Glu Pro Tyr Val Asp Val Thr Phe Thr Ile
210 215 220

Met Ile Arg Arg Arg Thr Leu Tyr Tyr Phe Phe Asn Leu Ile Val Pro
225 230 235 240

Cys Val Leu Ile Ser Ser Met Ala Leu Leu Gly Phe Thr Leu Pro Pro
245 250 255

Asp Ser Gly Glu Lys Leu Thr Leu Gly Val Thr Ile Leu Leu Ser Leu
260 265 270

Thr Val Phe Leu Asn Leu Val Ala Glu Thr Leu Pro Gln Val Ser Asp
275 280 285

Ala Ile Pro Leu Leu Gly Thr Tyr Phe Asn Cys Ile Met Phe Met Val
290 295 300

Ala Ser Ser Val Val Leu Thr Val Val Val Leu Asn Tyr His His Arg
305 310 315 320

Thr Ala Asp Ile His Glu Met Pro Gln Trp Ile Lys Ser Val Phe Leu
325 330 335

Gln Trp Leu Pro Trp Ile Leu Arg Met Ser Arg Pro Gly Lys Lys Ile
340 345 350

Thr Arg Lys Thr Ile Met Met Asn Thr Arg Met Arg Glu Leu Glu Leu
355 360 365

Lys Glu Arg Ser Ser Lys Ser Leu Leu Ala Asn Val Leu Asp Ile Asp
370 375 380

Asp Asp Phe Arg His Gly Pro Pro Pro Pro Asn Ser Thr Ala Ser Thr
385 390 395 400

B Gly Asn Leu Gly Pro Gly Cys Ser Ile Phe Arg Thr Asp Phe Arg Arg
405 410 415

Ser Phe Val Arg Pro Ser Thr Met Glu Asp Val Gly Gly Gly Leu Gly
420 425 430

Ser His His Arg Glu Leu His Leu Ile Leu Arg Glu Leu Gln Phe Ile
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Thr Ala Arg Met Lys Lys Ala Asp Glu Glu Ala Glu Leu Ile Ser Asp
450 455 460

Trp Lys Phe Ala Ala Met Val Val Asp Arg Phe Cys Leu Phe Val Phe
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Thr Leu Phe Thr Ile Ile Ala Thr Val Ala Val Leu Leu Ser Ala Pro
485 490 495

His Ile Ile Val Gln
500

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